

D. STEADMAN

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/556,178

DATE: 06/29/2001

TIME: 11:07:40

Input Set : N:\Crif3\RULE60\09556178.txt

Output Set: N:\CRF3\06292001\I556178.raw

SEQUENCE LISTING

C--> 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Bandman, Olga
 6 Lal, Preeti
 7 Guegler, Karl J.
 8 Shah, Purvi
 9 Corley, Neil C.

C--> 11 (ii) TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS

13 (iii) NUMBER OF SEQUENCES: 9

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 17 (B) STREET: 3174 Porter Dr.
 18 (C) CITY: Palo Alto
 19 (D) STATE: CA
 20 (E) COUNTRY: USA
 21 (F) ZIP: 94304

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Diskette
 25 (B) COMPUTER: IBM Compatible
 26 (C) OPERATING SYSTEM: DOS
 27 (D) SOFTWARE: FastSEQ for Windows Version 2.0

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/556,178

C--> 31 (B) FILING DATE: 20-Apr-2000

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 08/967,364
 35 (B) FILING DATE:

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Cerrone, Michael C.
 39 (B) REGISTRATION NUMBER: 39,132
 40 (C) REFERENCE/DOCKET NUMBER: PF-0417 US

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: 650-855-0555
 44 (B) TELEFAX: 650-845-4166

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 570 amino acids
 51 (B) TYPE: amino acid
 52 (C) STRANDEDNESS: single
 53 (D) TOPOLOGY: linear

55 (vii) IMMEDIATE SOURCE:

56 (A) LIBRARY: THPIPEB01
 57 (B) CLONE: 75871

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

64 Met Asn Val Val Phe Ala Val Lys Gln Tyr Ile Ser Lys Met Ile Glu
 65 1 5 10 15
 66 Asp Ser Gly Pro Gly Met Lys Val Leu Leu Met Asp Lys Glu Thr Thr

Paper No. 4
 DJS 06/29/01

ENTERED

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PATENT APPLICATION: US/09/556,178

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```

67          20          25          30
68 Gly Ile Val Ser Met Val Tyr Thr Gln Ser Glu Ile Leu Gln Lys Glu
69          35          40          45
70 Val Tyr Leu Phe Glu Arg Ile Asp Ser Gln Asn Arg Glu Ile Met Lys
71          50          55          60
72 His Leu Lys Ala Ile Cys Phe Leu Arg Pro Thr Lys Glu Asn Val Asp
73          65          70          75          80
74 Tyr Ile Ile Gln Glu Leu Arg Arg Pro Lys Tyr Thr Ile Tyr Phe Ile
75          85          90          95
76 Tyr Phe Ser Asn Val Ile Ser Lys Ser Asp Val Lys Ser Leu Ala Glu
77          100          105          110
78 Ala Asp Glu Gln Glu Val Val Ala Glu Val Gln Glu Phe Tyr Gly Asp
79          115          120          125
80 Tyr Ile Ala Val Asn Pro His Leu Phe Ser Leu Asn Ile Leu Gly Cys
81          130          135          140
82 Cys Gln Gly Arg Asn Trp Asp Pro Ala Gln Leu Ser Arg Thr Thr Gln
83          145          150          155          160
84 Gly Leu Thr Ala Leu Leu Leu Ser Leu Lys Lys Cys Pro Met Ile Arg
85          165          170          175
86 Tyr Gln Leu Ser Ser Glu Ala Ala Lys Arg Leu Ala Glu Cys Val Lys
87          180          185          190
88 Gln Val Ile Thr Lys Glu Tyr Glu Leu Phe Glu Phe Arg Arg Thr Glu
89          195          200          205
90 Val Pro Pro Leu Leu Leu Ile Leu Asp Arg Cys Asp Asp Ala Ile Thr
91          210          215          220
92 Pro Leu Leu Asn Gln Trp Thr Tyr Gln Ala Met Val His Glu Leu Leu
93          225          230          235          240
94 Gly Ile Asn Asn Asn Arg Ile Asp Leu Ser Arg Val Pro Gly Ile Ser
95          245          250          255
96 Lys Asp Leu Arg Glu Val Val Leu Ser Ala Glu Asn Asp Glu Phe Tyr
97          260          265          270
98 Ala Asn Asn Met Tyr Leu Asn Phe Ala Glu Ile Gly Ser Asn Ile Lys
99          275          280          285
100 Asn Leu Met Glu Asp Phe Gln Lys Lys Lys Pro Lys Glu Gln Gln Lys
101          290          295          300
102 Leu Glu Ser Ile Ala Asp Met Lys Ala Phe Val Glu Asn Tyr Pro Gln
103          305          310          315          320
104 Phe Lys Lys Met Ser Gly Thr Val Ser Lys His Val Thr Val Val Gly
105          325          330          335
106 Glu Leu Ser Arg Leu Val Ser Glu Arg Asn Leu Leu Glu Val Ser Glu
107          340          345          350
108 Val Glu Gln Glu Leu Ala Cys Gln Asn Asp His Ser Ser Ala Leu Gln
109          355          360          365
110 Asn Ile Lys Arg Leu Leu Gln Asn Pro Lys Val Thr Glu Phe Asp Ala
111          370          375          380
112 Ala Arg Leu Val Met Leu Tyr Ala Leu His Tyr Glu Arg His Ser Ser
113          385          390          395          400
114 Asn Ser Leu Pro Gly Leu Met Met Asp Leu Arg Asn Lys Gly Val Ser
115          405          410          415

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```

116 Glu Lys Tyr Arg Lys Leu Val Ser Ala Val Val Glu Tyr Gly Gly Lys
117           420           425           430
118 Arg Val Arg Gly Ser Asp Leu Phe Ser Pro Lys Asp Ala Val Ala Ile
119           435           440           445
120 Thr Lys Gln Phe Leu Lys Gly Leu Lys Gly Val Glu Asn Val Tyr Thr
121           450           455           460
122 Gln His Gln Pro Phe Leu His Glu Thr Leu Asp His Leu Ile Lys Gly
123           465           470           475           480
124 Arg Leu Lys Glu Asn Leu Tyr Pro Tyr Leu Gly Pro Ser Thr Leu Arg
125           485           490           495
126 Asp Arg Pro Gln Asp Ile Ile Val Phe Val Ile Gly Gly Ala Thr Tyr
127           500           505           510
128 Glu Glu Ala Leu Thr Val Tyr Asn Leu Asn Arg Thr Thr Pro Gly Val
129           515           520           525
130 Arg Ile Val Leu Gly Gly Thr Thr Val His Asn Thr Lys Ser Phe Leu
131           530           535           540
132 Glu Glu Val Leu Ala Ser Gly Leu His Ser Arg Ser Lys Glu Ser Ser
133           545           550           555           560
134 Gln Val Thr Ser Arg Ser Ala Ser Arg Arg
135           565           570

```

137 (2) INFORMATION FOR SEQ ID NO: 2:

139 (i) SEQUENCE CHARACTERISTICS:

140 (A) LENGTH: 2342 base pairs

141 (B) TYPE: nucleic acid

142 (C) STRANDEDNESS: single

143 (D) TOPOLOGY: linear

145 (vii) IMMEDIATE SOURCE:

146 (A) LIBRARY: THPIPEB01

147 (B) CLONE: 75871

149 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

151 GGACCTCGCG TCGGGCCAAC AGACTGCGGG GTTAATTTAG CCAGACACGT GGGCGGGAAG      60
152 GGCTGTAGGG TACTTGTCAA TTCGCGGCCA TGAACGTGGT TTTTGCTGTG AAGCAGTACA      120
153 TTTCCAAAAT GATAGAGGAC AGCGGGCCTG GTATGAAAGT ACTTCTCATG GATAAAGAGA      180
154 CGACTGGCAT AGTGAGTATG GTATACACAC AATCGGAGAT TCTACAGAAG GAAGTGTACC      240
155 TCTTTGAACG CATCGATTCT CAAAATCGAG AGATCATGAA ACACCTGAAG GCAATTTGTT      300
156 TTCTTCGACC TACAAAGGAG AATGTGGATT ATATTATTCA GGAGCTCCGA AGACCCAAAT      360
157 ACACTATATA TTTCATTTAT TTCAGTAATG TGATCAGCAA GAGTGACGTG AAGTCATTGG      420
158 CTGAAGCTGA TGAACAGGAA GTTGTGGCTG AGGTTTCAGGA ATTTTATGGT GATTACATTG      480
159 CTGTGAACCC ACATTTGTTT TCCCTCAATA TTTTGGGTTG CTGCCAGGGT CGAAATTGGG      540
160 ATCCAGCCCA GCTATCTAGA ACAACTCAAG GGCTTACAGC TCTCCTTTTA TCTCTGAAGA      600
161 AGTGTCCCAT GATTCGTTAT CAGCTCTCAT CAGAGGCAGC AAAGAGACTT GCAGAGTGCG      660
162 TTAAGCAAGT GATAACTAAA GAATATGAAC TGTTTGAATT CCGTCGGACA GAGGTTCCCTC      720
163 CATTGCTCCT TATTTTAGAT CGCTGTGATG ATGCCATCAC CCCATTGCTA AACCAGTGGA      780
164 CATATCAGGC CATGGTCCAC GAACTACTAG GCATAAACAA CAATCGGATT GATCTTTCCA      840
165 GAGTGCCGGG AATCAGTAAA GACTTAAGAG AAGTGGTCCT ATCTGCTGAA AATGATGAAT      900
166 TCTATGCTAA TAATATGTAC CTGAACTTTG CTGAGATTGG TAGCAATATA AAGAATCTCA      960
167 TGGAAGATTT TCAGAAGAAG AAACCAAAAG AACAGCAAAA ACTAGAATCA ATAGCAGACA     1020
168 TGAAGCGGTT TGTGAGAAT TATCCACAGT TCAAGAAAAT GTCTGGGACT GTTTCAAAGC     1080
169 ATGTGACAGT GGTGGAGAA CTGTCTCGAT TGGTCAGTGA ACGGAATCTG CTGGAGGTTT     1140

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```

170 CAGAGGTTGA GCAAGAACTG GCCTGTCAAA ATGACCATTG TAGTGCTCTC CAGAATATAA 1200
171 AAAGGCTTCT GCAGAACCCC AAAGTGACAG AGTTTGATGC TGCCCGCCTG GTGATGCTTT 1260
172 ATGCTTTACA TTATGAGCGA CACAGCAGCA ATAGCCTGCC AGGACTAATG ATGGACCTCA 1320
173 GGAATAAAGG TGTTCCTGAG AAGTATCGAA AGCTCGTGTC TGCAGTTGTT GAATATGGTG 1380
174 GTAAACGAGT CAGAGGAAGT GACCTCTTCA GCCCCAAAGA TGCTGTGGCT ATCACCACAAAC 1440
175 AATTCCTCAA AGGACTGAAG GGAGTAGAAA ATGTATATAC ACAGCATCAA CCTTTCCTAC 1500
176 ATGAAACCCCT GGATCATCTC ATCAAAGGAA GGCTTAAGGA AAACCTATAT CCTTATTTAG 1560
177 GCCCCAGCAC ACTCAGAGAC AGACCTCAGG ATATCATTTG GTTTGTAAAT GGAGGAGCCA 1620
178 CCTATGAAGA GGCTCTAACA GTTTATAACC TGAACCGCAC CACTCCTGGA GTGAGGATTG 1680
179 TCCTGGGAGG CACCACAGTG CACAACACGA AAAGTTTCCT AGAGGAAGTT CTGGCTTCTG 1740
180 GACTGCACAG CCGAAGCAAG GAGAGCTCTC AAGTCACATC AAGGTCAGCG AGCAGAAGAT 1800
181 GAAACGGTGG TTGGGGGAAG GGCACAGCTT CCTCTCTTGT CCCCCTACA GGTTTTCCCT 1860
182 ACTAAACAAA GGTGTTGGAG AGCAGCTTTG GGTTCTGTGC TGGTTGTTAG AACTCATCTC 1920
183 CAGGTAGCCC ACGGATACGT GGTGAGCACA GACACAAGAC TCCCAGAGTT GTCCTAACAA 1980
184 TAAGTCTGAG CCCACTCTCA CCCACTTTTC TCCGGTAGTC TTTATGTATC TGTTAGCACA 2040
185 ATCACTTCAG TTACTGATGA ATTTTGTGG GATCTGACTT GGGGAAAGGG TTATCAGAGC 2100
186 CTAGAGGGGC TTAAAAAGTA ATCATTTGAT GTACATACCA CACTCCTTGG CTTCTTTTCT 2160
187 CTTCCCTTAA CCCTTTCTGC TTTTCATTAA CCACATTCCT GCACAACCTCA TTTCTGAAAA 2220
188 CCTACCATGT TTCTTTACAG AGCCATCCAA AAATTTTTTG TCCCTACATA GCAATTTTCT 2280
189 GTGGCACTGA GAAACCATGT ATGACCACAA TAAAAATCCA TTTTGTGAAA GGAAAAAAA 2340
190 AA 2342

```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: 2056691

(B) CLONE: BEP1NOT01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

206 Met Lys Ile Trp Thr Ser Glu His Val Phe Asp His Pro Trp Glu Thr
207 1 5 10 15
208 Val Thr Thr Ala Ala Met Gln Lys Tyr Pro Asn Pro Met Asn Pro Ser
209 20 25 30
210 Val Val Gly Val Asp Val Leu Asp Arg His Ile Asp Pro Ser Gly Lys
211 35 40 45
212 Leu His Ser His Arg Leu Leu Ser Thr Glu Trp Gly Leu Pro Ser Ile
213 50 55 60
214 Val Lys Ser Leu Ile Gly Ala Ala Arg Thr Lys Thr Tyr Val Gln Glu
215 65 70 75 80
216 His Ser Val Val Asp Pro Val Glu Lys Thr Met Glu Leu Lys Ser Thr
217 85 90 95
218 Asn Ile Ser Phe Thr Asn Met Val Ser Val Asp Glu Arg Leu Ile Tyr
219 100 105 110
220 Lys Pro His Pro Gln Asp Pro Glu Lys Thr Val Leu Thr Gln Glu Ala
221 115 120 125
222 Ile Ile Thr Val Lys Gly Val Ser Leu Ser Ser Tyr Leu Glu Gly Leu
223 130 135 140

```

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224 Met Ala Ser Thr Ile Ser Ser Asn Ala Ser Lys Gly Arg Glu Ala Met
 225 145 150 155 160
 226 Glu Trp Val Ile His Lys Leu Asn Ala Glu Ile Glu Glu Leu Thr Ala
 227 165 170 175
 228 Ser Ala Arg Gly Thr Ile Arg Thr Pro Met Ala Ala Ala Ala Phe Ala
 229 180 185 190
 230 Glu Lys

233 (2) INFORMATION FOR SEQ ID NO: 4:

235 (i) SEQUENCE CHARACTERISTICS:

236 (A) LENGTH: 836 base pairs

237 (B) TYPE: nucleic acid

238 (C) STRANDEDNESS: single

239 (D) TOPOLOGY: linear

241 (vii) IMMEDIATE SOURCE:

242 (A) LIBRARY: 2056691

243 (B) CLONE: BEP1NOT01

245 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

247 GAGCGGGGCA GGGGCAGGTG TAGCCTCTGT GCCTCGTTGT CCCCTGGCGC TACCCGGACA 60
 248 TCTCTCAGGG TGCCGGCACC ATGAAGATCT GGACTTCGGA GCACGTCTTT GACCACCCGT 120
 249 GGGAAACTGT TACAACAGCT GCAATGCAGA AATACCCAAA CCCTATGAAC CCAAGTGTGG 180
 250 TTGGAGTTGA TGTGTTGGAC AGACATATAG ATCCCTCTGG AAAGTTGCAC AGCCACAGAC 240
 251 TTCTCAGCAC AGAGTGGGGA CTGCCTTCCA TTGTGAAGTC TCTTATTGGT GCAGCAAGAA 300
 252 CGAAAACATA TGTGCAAGAA CATTCTGTAG TTGATCCTGT AGAGAAAACA ATGGAACCTTA 360
 253 AATCTACTAA TATTTTATTT ACAACATGG TTTCAGTAGA TGAGAGACTT ATATACAAAC 420
 254 CACATCCTCA GGATCCAGAA AAAACTGTTT TGACACAAGA AGCCATAATT ACCGTGAAAG 480
 255 GAGTTAGCCT CAGCAGTTAC CTTGAAGGAC TGATGGCAAG TACGATATCC TCAAATGCTA 540
 256 GTAAAGGCCG AGAAGCAATG GAATGGGTAA TACATAAATT AAATGCTGAG ATTGAAGAAC 600
 257 TGACAGCCTC AGCAAGAGGA ACCATAAGGA CTCCAATGGC AGCAGCAGCG TTTGCAGAGA 660
 258 AGTGATCGTG ACAGTTGGTA GACAACATCG GGTACTCCAG GTCTCTCCAA ACTGACTATA 720
 259 TATTTATTTG TTATTTTAAA AATACAACTA TATTTTGGGT AGTTTTTTTT TTTTTTTTTT 780
 260 TTGATAAGTT GGTGTAAGGC TATGTGACTG ATCAAAACAG ATGCAGGGCC TCTAAA 836

262 (2) INFORMATION FOR SEQ ID NO: 5:

264 (i) SEQUENCE CHARACTERISTICS:

265 (A) LENGTH: 177 amino acids

266 (B) TYPE: amino acid

267 (C) STRANDEDNESS: single

268 (D) TOPOLOGY: linear

270 (vii) IMMEDIATE SOURCE:

271 (A) LIBRARY: HEAONOT03

272 (B) CLONE: 3086794

274 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

276 Met Glu Ala Leu Ile Leu Glu Pro Ser Leu Tyr Thr Val Lys Ala Ile
 277 1 5 10 15
 278 Leu Ile Leu Asp Asn Asp Gly Asp Arg Leu Phe Ala Lys Tyr Tyr Asp
 279 20 25 30
 280 Asp Thr Tyr Pro Ser Val Lys Glu Gln Lys Ala Phe Glu Lys Asn Ile
 281 35 40 45
 282 Phe Asn Lys Thr His Arg Thr Asp Ser Glu Ile Ala Leu Leu Glu Gly
 283 50 55 60

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/556,178

DATE: 06/29/2001

TIME: 11:07:42

Input Set : N:\CrF3\RULE60\09556178.txt

Output Set: N:\CRF3\06292001\I556178.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:11 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]